- 1 Sociodemographic factors modulate the spatial response of brown bears to vacancies created by
- 2 hunting.
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## Summary

- 1. There is a growing recognition of the importance of indirect effects from hunting on wildlife
- populations, e.g., social and behavioral changes due to harvest, which occur after the initial offtake.
- Nonetheless, little is known about how the removal of members of a population influences the spatial
- 27 configuration of the survivors.
- 28 2. We studied how surviving brown bears (*Ursus arctos*) used former home ranges that had belonged
- to casualties of the annual bear hunting season in southcentral Sweden (2007-2015). We used
- resource selection functions to explore the effects of the casualty's and survivor's sex, age, and their
- 31 pairwise genetic relatedness, population density, and hunting intensity on survivors' spatial responses
- 32 to vacated home ranges.
- 3. We tested the competitive release hypothesis, whereby survivors that increase their use of a killed
- bear's home range are presumed to have been released from intraspecific competition. We found
- 35 strong support for this hypothesis, as survivors of the same sex as the casualty consistently increased
- their use of its vacant home range. Patterns were less pronounced or absent when the survivor and
- casualty were of opposite sex.
- 4. Genetic relatedness between the survivor and the casualty emerged as the most important factor
- 39 explaining increased use of vacated male home ranges by males, with a stronger response from
- 40 survivors of lower relatedness. Relatedness was also important for females, but it did not influence
- 41 use following removal; female survivors used home ranges of higher related female casualties more,
- both before and after death. Spatial responses by survivors were further influenced by bear age,
- population density, and hunting intensity.
- 5. We have showed that survivors exhibit a spatial response to vacated home ranges caused by
- 45 hunting casualties, even in non-territorial species such as the brown bear. This spatial reorganization
- can have unintended consequences for population dynamics and interfere with management goals.

- 47 Altogether, our results underscore the need to better understand the short- and long-term indirect
- effects of hunting on animal social structure and their resulting distribution in space.

# 49 **Keywords**

- 50 Spatial response, kinship, competition, spatial reorganization, harvest, social structure, mortality, *Ursus*
- 51 arctos

#### Introduction

Hunting has important direct and indirect effects on wildlife populations (Milner, Nilsen & Andreassen 2007). By removing individuals, hunting creates vacancies in a population's social and spatial configuration (McComb *et al.* 2001). In response to this removal, surviving individuals may exhibit a spatial reorganization (Gese 1998; Leclerc *et al.* 2017), which in turn may affect social structure, reproduction, and ultimately population dynamics (Robinson *et al.* 2008; Cooley *et al.* 2009). It is therefore important to better understand the effects of hunting on the space use of surviving individuals for sustainable hunting practices.

One consequence of the removal of conspecifics (hereafter *casualties*) is the release of surviving individuals (hereafter *survivors*) from competition or social constraints (Maletzke *et al.* 2014; Loveridge *et al.* 2016). Competitive release may manifest itself in the increased use of a casualty's former home range (HR; hereafter *vacancy*) by survivors (Gese 1998; Goodrich *et al.* 2010), i.e. a spatial response, which in turn could be influenced by several sociodemographic factors (Maletzke *et al.* 2014; Loveridge *et al.* 2016).

Sex is an important factor for determining life history strategies, social systems, and consequently population structure (Lott 1991; Bonenfant *et al.* 2002). Same-sex individuals compete for breeding opportunities or for resources necessary for reproduction (Clutton-Brock & Huchard 2013a). Sex-differences in morphology and habitat selection likely decrease intersexual competition, enabling the sharing of space and mating opportunities (e.g. Zabala, Zuberogoitia & Martinez-Climent 2007). Therefore, the removal of same-sex individuals has the potential to induce stronger spatial responses by survivors than the removal of opposite-sex individuals, if intrasexual competition is a spatially limiting factor for a given sex (e.g. Nelson 1995).

Kin selection theory states that the degree of genetic relatedness can influence competition among individuals (Hamilton 1964). Higher genetic relatedness between individuals has been linked to higher HR overlap and increased spatial aggregations (Ratnayeke, Tuskan & Pelton 2002; Wronski &

Apio 2005). Within these socio-spatial relationships, relatedness has been shown to increase reproductive output, foraging efficiency, and tolerance (Pusenius *et al.* 1998; Wronski & Apio 2005; Wright *et al.* 2016). The removal of kin from a population in social species can lower the competitive ability of the surviving kin to gain access to space and associated resources, as well as breeding opportunities (McComb *et al.* 2001; Clutton-Brock & Huchard 2013b). In comparison, unrelated survivors may benefit from removals, which may result in stronger spatial responses toward vacancies belonging to nonkin. Kin-based aggregations in mammals are more common in females than males, due to female-biased philopatry (Waser & Jones 1983). Furthermore, there is increasing evidence that female space use among solitary carnivores is linked to mother-daughter home range overlap, a pattern not observed between mothers and sons (Fattebert *et al.* 2015; Fattebert *et al.* 2016). Therefore, the influence of relatedness on survivors' spatial responses may differ between the sexes and be stronger for females in philopatric species.

Additional factors commonly modulate the level of intra- and intersexual competition in space use. For example, age is often associated with dominance status (Clutton-Brock & Huchard 2013a), reproductive success (e.g. King, Festa-Bianchet & Hatfield 1991), and access to resources (McComb et al. 2001). The removal of older, dominant individuals from a population allows nearby survivors to exploit resources previously denied to them either directly through aggression or indirectly through increased use (Pilfold, Derocher & Richardson 2014) of the killed animal's HR. Furthermore, older nearby survivors may be able to better take advantage of vacancies (i.e., HRs of a removed individual), as seen in Seychelles warblers (*Acrocephalus sechellensis*) (Eikenaar et al. 2008). Increasing population density can increase competition for food resources and breeding opportunities (e.g. McLoughlin et al. 2006). The removal of an individual decreases direct competition experienced by a nearby survivor, but the magnitude of this effect may depend on population density. At higher densities, the spatial response of a nearby survivor can be limited, due to prevailing spatial competition among a higher number of other survivors (Leclerc et al. 2017). At the same time, populations with

higher hunting intensities or individual turnover are typically less stable in terms of social structure, which can increase spatial responses (Porter *et al.* 1991; Comer *et al.* 2005).

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Examining the combined effects of sociodemographic factors on survivors' spatial responses to the removal of conspecifics requires detailed individual-based data. Most studies on the effects and mechanisms of removal on spatial reorganization have been conducted on territorial birds, many of which were not hunted populations (e.g. Eikenaar *et al.* 2008). The paucity of knowledge on spatial responses in mammals and those which are hunted is likely due to the scarcity of individual-based data needed to investigate their social structure (Clutton-Brock & Sheldon 2010).

Here we use detailed individual-based, social, spatial and genetic data on brown bears (Ursus arctos) to explore the effects of removing individuals in a hunted population on survivors' spatial responses. The brown bear is a large solitarily-living carnivore (Steyaert et al. 2012). However, related females form aggregations (Støen et al. 2005), and HRs of both sexes vary similarly according to food availability and population density (Dahle & Swenson 2003). Leclerc et al. (2017) found for male brown bears that survivors' increased use of casualties' HRs was modulated by bear age, population density, and hunting intensity. This study builds upon those findings to explore the responses in both sexes and evaluate whether kinship between casualties and survivors modulates the post-hunt spatial reorganization. By considering a casualty's former home range as an area containing resources, we used resource selection functions (RSFs) (Manly et al. 2002) to investigate which factors affect the spatial responses of survivors during the two years following the removal of a nearby individual. Based on the competitive release hypothesis, we predicted that: (P1a) survivors would increase their use of a casualty's HR and (P1b) this increase would be stronger when survivors and casualties are of the same sex. (P2) Genetic relatedness should be negatively correlated with survivors' increase in use of casualties' HRs if both are females, but not if they are males or bears of the opposite sex. (P3) Ages of both survivors and casualties would be positively related to a survivor's increase in use of a casualty's

HR. (P4) Population density would be negatively related to a survivor's increase in use of a casualty's HR, whereas (P5) hunting intensity will be positively related to increases in use.

#### **Materials and Methods**

The study area is located in southcentral Sweden (61°N, 15°E) and is composed of bogs, lakes, and intensively managed and mixed-aged forest stands. Between 1985-2015, we captured 499 brown bears from a helicopter using a remote drug delivery system (Dan-Inject®, Børkop, Denmark) (Fahlman *et al.* 2011). All captures and handling were approved by the Swedish Board of Agriculture, Uppsala Ethical Committee on Animal Experiments, and the Swedish Environmental Protection Agency. We determined the bears' sex at capture and extracted a premolar tooth for age determination (Matson 1993) from individuals not captured as a yearling (n = 181). Starting in 2003, we equipped bears with GPS collars (GPS Plus; Vectronic Aerospace GmbH, Berlin, Germany) programmed to relocate a bear with varying schedules (≤1 hour). In addition, we acquired data on location, sex, and age (determined as above) for all known dead brown bears in Sweden between 1981-2014 (n = 3,960), of which 83% was caused by legal hunting.

#### MODEL DEVELOPMENT

We assumed that a vacancy created through the removal of a conspecific was a spatially explicit 'resource' or a collection of resources available to remaining survivors. We used resource selection functions (RSFs; Manly *et al.* 2002) to determine whether survivors showed a spatial response over time to vacancies. RSFs contrast relocations of use and those randomly available, while explaining the pattern of use with a set of covariates, e.g., whether a location falls inside or outside a specific area or a casualty's former HR in this case. We coded the dependent variable as either a real GPS (= 1) or a simulated, randomly created (= 0) relocation; the latter represented the extent of use by neighboring bears of the casualty's home range under the null hypothesis absent of competitive exclusion. We used generalized linear mixed models (GLMM) with a logit link to assess the influence of sex on spatial

responses (Step I). Then, to simplify model complexity, we evaluated how spatial responses was modulated by age, pairwise relatedness, density index, and hunting intensity separately by casualty-survivor sex combination (Step II).

#### LOCATION DATA

We only included adult bears (≥ 4 year-olds; Støen *et al.* 2006) in the analysis to avoid potential confounding effects of dispersing bears on the spatial response to harvest. We removed GPS fixes with dilution of precision values >10 to increase spatial accuracy (D'Eon & Delparte 2005). To reduce autocorrelation caused by a lack of independence among successive GPS positions, we used a 6-hour minimum interval between successive positions (yielding a maximum of 4 relocations per bear/day). We excluded bears that had <75% of days with relocations during May 1 − August 21 (after den exit until the start of hunting) in a given year from 2007-2015 to have adequate coverage of the bear's nondenning period. We defined casualties' HRs with the 95<sup>th</sup> percentile isocline from a kernel density distribution, using the 'reference' bandwidth (*ad hoc* method) and a fixed kernel in the R package 'adehabitatHR' (Calenge 2006).

#### **COVARIATE DESCRIPTION**

We extracted an annual population density index for each casualty. This index was derived using spatially-referenced genetic data obtained from county-level scat collections in Sweden. Individual bears were identified from feces using six microsatellites (see Bellemain *et al.* 2005; Kindberg *et al.* 2011). Scat collections occurred in different years among counties and collection was not spatially homogenous. Therefore, we chose a grid size of 10x10 km cells and adopted the method of Jerina et al. (2013) to sum the weighted values of an individual bear's (multiple) scats across this spatial grid. An individual's scat count was weighted  $(1/\sqrt{n})$  according to the number of samples collected, so that the sum of the weighted values was equal among all individuals (Jerina *et al.* 2013). The weighted scat values were then summed by cell at the county level, after which the county-level distribution was annually corrected using county-level trends of the Large Carnivore Observation Index

(LCOI; provided by the Swedish Association for Hunting and Wildlife Management; Kindberg, Ericsson & Swenson 2009; Kindberg *et al.* 2011) during the study period. All county grids were then summed and joined to produce an annual density index for the study area for 2007-2015. The resulting grids were then smoothed using a 3x3 cell moving window (30x30 km) (see Appendix S1). Density index values were extracted at the casualties' HR centroids.

We used 16 autosomal microsatellites (Table S1; Støen *et al.* 2005) to construct a pedigree and to calculate relatedness estimates between individuals (Lynch & Ritland 1999). This pedigree (Table S2) included genetics from captured and recovered dead bears (N = 1,614). To estimate relatedness, we chose Lynch and Ritland's (1999) estimator, because it has shown the highest correlation with theoretical relatedness values from a simulated pedigree of known relationships compared to other estimators (Csillery *et al.* 2006). We used the relatedness estimates calculated using the microsatellites rather than from the pedigree, because it avoided information loss caused by missing parental assignments in the pedigree (Zeyl *et al.* 2009). Additionally, the mean values of the relatedness estimates closely matched the theoretical relatedness in our pedigree (Fig. S1).

We calculated a proxy for hunting intensity based on the number of dead bears located within a 40-km buffer of a casualty's HR centroid 3 years prior to its death. We only used dead bears of the same sex as the casualty in this calculation, to keep the additive effect on changes in the spatial response by survivors consistent by sex (see Step I under *Model Structure*).

For each casualty, we 1) determined its annual 95% kernel HR for the year in which it was killed and 2) calculated a 40-km radius circular buffer centered on its HR centroid (Fig. 1). We chose the 40-km buffer radius, because it is the distance within which most HR centroids of successful mates occur (Bellemain *et al.* 2006) and it is beyond the range of a dead male's influence on sexually-selected infanticide (SSI) and cub survival (Gosselin *et al.* 2017). We used the GPS relocations of all survivors and that of the casualty within the circular buffer during the year of the casualty's death to 3) calculate a 95% kernel isocline (hereafter sampling space), and 4) we determined if relocations of each survivor

were inside or outside the casualty's HR for a given year (see period below). For each survivor, we 5) generated the same number of random as real GPS relocations within the sampling space and 6) assigned them the same attributes (i.e. sex and age, population density, pairwise relatedness, and hunting intensity) as the observed relocations. We 7) determined if the random relocations were inside or outside the casualty's HR. We repeated steps 4-7 for a 3-year period (Y0 = before the casualty bear died, Y1 = first year after death, and Y2 = second year after death) while keeping the sampling space constant from that derived in Y0. The sampling space was kept constant, because we did not want to create a sampling landscape that had never existed by varying according to the former home range of a shot bear with that of future positions from its neighbors.

#### MODEL STRUCTURE

Step I: effect of sex on survivors' spatial responses

We tested the sex effect on survivor responses (Step I: sex-effect model). We compared candidate models of increasing complexity (Table 1), with the complete model consisting of a 4-way interaction including the casualty's sex (2 levels), the survivor's sex (2 levels), the period (factor with 3 levels: Y0, Y1, and Y2; see Fig. 1), as well as a dummy variable representing whether the relocations were inside (= 1) or outside (= 0) the casualty's HR. To control for unequal sample sizes among individuals and possible temporal collinearity within pairs, we nested the survivor's ID into the casualty's ID as a random effect on the intercept. Additionally, we used the year of the survivor's response as a random intercept to account for possible interannual environmental effects on survivors' responses. The sex-effect dataset (Step I) consisted of 26 casualties (14 females, 12 males), 26 survivors (with a mean of six female and two male survivors per casualty), yielding 216 casualty and survivor dyads over a three-year period, and 601,398 survivor relocations used for analyses.

Step II: additional factors modulating survivors' spatial responses

Based on the results of Step I, we reduced model complexity and controlled for the sex effect in Step II by creating separate candidate models for all sex combinations of casualty-survivor bears. We

evaluated which factors (age, pairwise relatedness, density index, hunting intensity) were most important in modulating the patterns observed in Step I. These model data sets consisted of 38,266 relocations for male-male (11 casualties; 7 survivors), 263,838 relocations for male-female (11 casualties; 15 survivors), and 257,420 relocations for female-female (14 casualties; 19 survivors). We built candidate models of increasing complexity, with the complete model consisting of additive factors each interacting with the dummy variables "Inside" and "Period" (see Table 2). We used the same random effects structure as in Step I. For all models tested in Steps I and II, the variance inflation factor (VIF) values for all variables were < 3 (Zuur, Ieno & Elphick 2010).

## MODEL SELECTION AND VALIDATION

We used the Bayesian Information Criterion (BIC) to select the "best model" for each Step I and Step II model results, i.e., the model that best fit the data while concurrently penalizing the number of parameters estimated in the model fitting process. We assessed the relative importance of variables within the best models by dropping each variable of the model and monitoring the  $\Delta$ BIC. The larger the relative increase in BIC compared to the best model, the more important we considered the variable. We assessed the robustness of our results by varying the kernel isocline (i.e. 75%, 90%, and 95%) of the sampling space and compared model predictions across isoclines (*sensu* Bischof *et al.* 2016). We used R 3.2.4 for all statistical analyses (R Development Core Team 2016).

## Results

## EFFECT OF SEX ON SURVIVORS' SPATIAL RESPONSES TO VACANCIES

The complete model, keeping all fixed terms and interactions, had the best fit (Table 1 and S3). It suggested that survivors increased their use of a casualty's HR, especially if they were of the same sex. However, male survivors did not increase their use of a female casualty's HR (Fig. 2). A male survivor was 1.03 (95% CI: 0.89 – 1.20) and 1.42 (95% CI: 1.22 – 1.64) times more likely to use a male casualty's HR during the first (Y1) and second (Y2) year after the casualty's death (Y0),

respectively (Fig. 2). A female survivor was 1.30 (95% CI: 1.17 – 1.44) and 1.55 (95% CI: 1.40 – 1.72) times more likely to use a female casualty's HR during the first (Y1) and second (Y2) year after the casualty's death (Y0), respectively. We detected no clear temporal trends in casualties and survivors belonging to different sexes. For example, a female survivor was 1.14 (95% CI: 1.08 – 1.20) more likely to use a male casualty 's HR in the first year after his death (Y1), but this dropped to near baseline level (Y0), i.e., 1.07 (95% CI: 1.01 – 1.13) during the second year (Y2). Most patterns were robust against varying isoclines (75%, 90%, and 95%) on the sampling space, with the exception of male-male spatial responses at the 75% isocline, which were no longer detectable at this scale (Fig. S2). As all other spatial responses were virtually the same across isoclines, we only present the 95% isocline results in Step II.

#### ADDITIONAL FACTORS MODULATING SURVIVOR SPATIAL RESPONSES TO VACANCIES

We excluded the female-male dyads for Step II analyses, because male survivors did not change their use of female casualties' HRs. In decreasing order of importance, the best model for the malemale model retained relatedness ( $\Delta BIC = 363$ ), the survivor's age ( $\Delta BIC = 302$ ), and hunting intensity ( $\Delta BIC = 18$ ) (Table 2 and S4). The best female-female model kept relatedness ( $\Delta BIC = 2371$ ), the casualty's age ( $\Delta BIC = 290$ ), and hunting intensity ( $\Delta BIC = 106$ ) (Table 2 and S5). The most important variable for the male-female combination was density ( $\Delta BIC = 3544$ ), followed by the survivor's age ( $\Delta BIC = 2792$ ), and hunting intensity ( $\Delta BIC = 1780$ ) (Table 2 and S6).

In both male-male and female-female dyads, higher relatedness (ranging from -0.31 to -0.17 and from -0.41 to 0.44, respectively) explained the higher magnitude of a survivor's use of a casualty's HR (Fig. 3a and b). The positive change in a female survivor's use of a female casualty's HR was similar across periods for both low (25<sup>th</sup> percentile) and high relatedness (75<sup>th</sup> percentile) (Fig. 3b). In contrast, male survivors with lower relatedness to a male casualty showed a stronger increase in use of its HR from Y1 to Y2 than male survivors of higher relatedness (Fig. 3a). Furthermore, the increase in use of a male casualty's HR from Y1 to Y2 was stronger when male survivors were older and in areas of high

hunting intensity (Fig. 3c and 4a). Similarly, the increase in use of a female casualty's HR by female survivors was stronger in areas of higher hunting intensity (Fig. 3d). There was no increase in use of a female casualty's HR if the female casualty was older, whereas the increase was strong when the casualty was younger (Fig. 4b). Older female survivors in low density with high hunting intensity increased their use of a male casualty's HR in Y1, but this was reduced or reversed in Y2 (Fig. 4c, 4d, and 4e). The most common retained variable was hunting intensity, which was generally associated with increased use of a casualty's HR (Fig. 3c, 3d and 4e). For all models, the random intercepts on casualty ID and on survivor ID nested in casualty ID had a variance below 0.02. Furthermore, the random intercept on year was virtually zero (< 0.001) for all models.

#### **Discussion**

The removal of bears by hunters had a pronounced effect on the spatial configuration of survivors. We found that spatial responses to hunter-created vacancies and the role of modulating factors was highly dependent on sex of survivors and casualties. In support of our predictions, the pattern of increased use of a casualty's HR (P1a) by same-sex survivors (P1b) was best explained by intrasexual competition. Intrasexual HR exclusion often contrasts with intersexual HR overlap in territorial species (e.g. Persson, Wedholm & Segerström 2009), presumably due to stronger competition within the sexes to maximize mating opportunities and access to other resources (Clutton-Brock & Huchard 2013b). Some territorial species reduce intersexual competition through a seasonally flexible social organization (e.g. Erlinge & Sandell 1986) or sexual differences in habitat selection and behaviors (e.g. Zabala, Zuberogoitia & Martinez-Climent 2007), which are linked to sexual dimorphism (Beerman *et al.* 2015).

It is noteworthy that we detected these pronounced spatial patterns in a nonterritorial species.

Competition for resources in nonterritorial, solitary-living species, such as the brown bear, is harder to detect than in territorial species, because inter- and intrasexual HR overlap is common. Therefore fewer

studies on competition exist in these species (Pilfold, Derocher & Richardson 2014), but observed segregation in habitat selection between the sexes within areas of HR overlap implies competition or at least conflicts of interests (e.g. SSI; Steyaert *et al.* 2016). Furthermore, resource availability can vary annually within HRs, which could modulate an individual bear's decision whether to increase its use of a vacancy. However, the random intercept on year accounted for very little variance across all models, giving little evidence that interannual variation of resources had an effect on the spatial response of survivors to vacancies in our study.

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Although bears are generally considered nonterritorial, dominance hierarchies have been observed around clustered food sources, like salmon (Oncorhynchus spp.) spawning rivers and garbage dumps (e.g. SSI; Gende & Quinn 2004; Peirce & Van Daele 2006). Furthermore, territorial behavior and dominance may play a larger role in space use in both sexes in the study population than previously thought (Støen et al. 2005; Zedrosser et al. 2007; Ordiz et al. 2008). This is most pronounced in female kin aggregations, where females may exclude unrelated females through "social fences," i.e., increasing density results in increasing aggression between members of different female aggregations during dispersal (Hestbeck 1982; Støen et al. 2005; Odden et al. 2014). Our results did not provide evidence for social fences in modulating spatial responses, as bear density was not retained in the best model for the female-female dyad and relatedness did not explain changes in the magnitude of a female survivor's use of a female casualty's HR over time. It is likely that vacancies are filled by both nearby survivors as well as immigrant dispersers (e.g. Benson, Chamberlain & Leopold 2004). Our study included adults that had already dispersed and established HRs, so kin-based social fences could still influence dispersal between female aggregations. Contrary to our prediction (P2), low relatedness between females did not correspond to a stronger increase in use of a female casualty's HR across time. Higher relatedness did explain the higher magnitude of use of female vacancies by survivors of the same sex, which corresponds with kin-based aggregations of females due to philopatry (Støen et al.

2005; Støen *et al.* 2006). However, it remains unknown if the presence of nearby female kin results in fitness benefits (Støen *et al.* 2005).

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Surprisingly, we found that relatedness best explained a male survivor's increase in use of a male casualty's HR, with lower relatedness explaining larger increases in use in the second year following death. This contrasts our prediction (P2), that kinship would only be important for females. We confirmed that male spatial structure did not exhibit kin-based aggregations, as seen in females (Fig. S3; Støen et al. 2005), implying that male kinship may be important at the local level, but not at a larger spatial scale. Even without kin-based aggregations among males, male-male interactions among solitary carnivores are likely more complex than previously thought (e.g. Elbroch et al. 2016). For example, males of the solitary-living fossa (Cryptoprocta ferox) can remain solitary or form stable associations, with kinship among other factors proposed as explanations (Lührs & Kappeler 2013). In our study, it is possible that male-male kinship created contexts in which males exhibited higher tolerance for one another at the local scale, as evidenced by stronger apparent competitive release of survivors to casualties of lower relatedness. However, we treat this interpretation with caution, because the range of estimated relatedness values among male dyads in our study was lower (from -0.31 to 0.17) relative to female (from -0.41 to 0.44) and male-female (from -0.31 to 0.3) dyads, indicating that patterns in male dyads may not be biologically significant. The smaller range for male dyads is likely a result of male-biased dispersal (Zedrosser et al. 2007).

In contrast to our prediction (P3), female survivors increased their use of the HRs of younger female casualties, but not those of older female casualties. We suggest two alternative explanations: (1) that the location of younger and older female HRs occurred in areas of low and high HR overlap, respectively (sensu Maletzke *et al.* 2014), or (2) that surviving females consistently avoided older female HRs even after death. Neither explanation was supported, as a post-hoc analysis showed that HR overlap between individual females and their female neighbors was constant across individual females' ages (Fig. S4). Nevertheless, areas of higher female HR overlap may be more resilient to

spatial responses following the removal of female conspecifics, as the costs of responding spatially may outweigh its benefits. One example is increased predation mortality due to site unfamiliarity (e.g. Forrester, Casady & Wittmer 2015). Spatial responses of male bears to harvest-induced vacancies is consistent with the risk of SSI (Leclerc *et al.* 2017), but it is unclear how female spatial responses, i.e., their exploration of previously denied resources, may enhance the risk of SSI. Although female bears modulate SSI risk through differential habitat selection, the relative risk of SSI has not been studied at the HR scale (Steyaert *et al.* 2016). A female exhibiting high HR overlap with a killed female may have both limited costs in a spatial response, due to preexisting familiarity with her surroundings, and limited benefits, due to already optimally used resources. However, through gradual expansion, females can also increase their access to other resources, such as space for future philopatic offspring, as seen in striped mice, *Rhabdomys pumilio* (Schradin *et al.* 2010).

As predicted (P3), older males exhibited a stronger increase in their use of a male vacancy than younger males, perhaps due to differences in experience. Male bears have larger HRs than females and potentially also larger cognitive maps (Perdue *et al.* 2011; Noyce & Garshelis 2014). Greater experience and spatial knowledge may improve abilities to find and relocate resources, as seen in African elephants (*Loxodonta africana*) (McComb *et al.* 2001). In American black bears (*U. americanus*), Noyce and Garshelis (2014) found that migratory movement patterns appeared to be based on social cues, with males as leaders in paving the way toward important first-come, first-served food resources. Although age was not important in their study, age and experience play a role in social learning for other species (Galef & Laland 2005). Furthermore, dominant individuals might be more successful at taking over novel HR vacancies than subordinates, e.g. in side-blotched lizards (*Uta stansburiana*) (Fox, Rose & Myers 1981). The same first-come, first-served process may work with HRs as they become available, e.g. due to the death of conspecifics, with an older/dominant survivor taking advantage of newly available resources.

Our prediction (P4) that density would be negatively related to increases in use of vacancies by survivors was confirmed for female survivors and male casualties, but was absent for all other casualty-survivor sex combinations. Low density areas have lower concentrations of females and were near the periphery of our population (Swenson, Sandegren & Soderberg 1998). The strong increase in use of male vacancies by females in low-density areas might suggest that females can take advantage of resources previously dominated by males at the population periphery. Conversely, females at high densities did not increase their use of male vacancies, so density may represent a larger response of nearby survivors competing for this recently vacated HR. The absent effect of density in explaining spatial responses by same-sex survivors suggests that other context-dependent social factors (sex, relatedness, age), such as hunting intensity, are more important for a survivor's decision to respond spatially rather than the number of conspecifics surrounding it.

Higher hunting intensity provides more vacancies toward which nearby survivors can respond spatially (Leclerc *et al.* 2017). Although the spatial distribution of these vacancies available to survivors may vary, hunting intensity had (P5) a consistently positive relationship with the increased use of a vacancy by survivors for all casualty-survivor sex combinations depicting spatial responses. Furthermore, hunting intensity was the only factor retained in the best model for all sex combinations. Therefore, we found evidence for a consistent, additive effect of hunting intensity on a surviving animal's spatial response towards a vacancy, which suggests a long-term effect of hunting on the dynamics of HRs.

Management decisions, such as the degree of hunting intensity, appears to drive spatial responses of survivors and, therefore, likely alters competition for resources among survivors.

Furthermore, we suggest that solitary species may be more social, with a basis in kinship, and that male-male relationships may be more complex than previously considered. The spatial reorganization caused by hunting and potentially compounding effects of continued hunting on social structure could be an important consideration when developing plans for sustainable harvest of wildlife populations, or

for achieving other management goals, such as decreasing human-wildlife conflicts. Altogether, our results underscore the need to better understand the short- and long-term indirect effects of hunting on animal social structure and their resulting distribution in space, which, if not understood, could have unforeseen consequences on population parameters such as fitness and population growth (Frank *et al. in press*).

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### **Author Contribution Statement:**

SCF, ML, RB, JES, FR, FP, and AZ participated in the study design. SCF, ML, and RB carried out statistical analyses. AZ, JES, and FP secured funding. JES, AZ, and JK coordinated work in the Scandinavian Brown Bear Research Project. HGE and SBH provided expertise and work on the genetics. All authors contributed to the writing of the manuscript.

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# **Data Accessibility**

Data are available from the Dryad Digital Repository: doi:10.5061/dryad.m7m8n (Frank et al. 2017).

## **Table captions**

**Table 1.** Results of the candidate models tested to determine the spatial responses of surviving brown bears to the death of nearby hunter-killed bears (casualties). The number of parameters (K), log-likelihoods (LL), the change in BIC ( $\Delta$ BIC) from the best model, and the model weights ( $\omega$ ) are shown.

**Table 2.** Results of the candidate models tested to determine the effect of age, pairwise relatedness, density index, and hunting intensity in modulating the spatial responses of surviving brown bears (survivors; S) to the death of nearby hunter-killed bears (casualties; C). The number of parameters (K), log-likelihoods (LL), the change in BIC ( $\Delta$ BIC) from the best model, and the model weights ( $\omega$ ) are shown for each casualty-survivor combination.

Table 1.

Model	Variable*	K	LL	ΔΒΙϹ	ω
1	None	4	-416857	3512	0
2	$Inside \times Period$	9	-416120	2104	0
3	Casualty Sex $\times$ Inside $\times$ Period	15	-415877	1698	0
4	Survivor Sex $\times$ Inside $\times$ Period	15	-415304	552	0
5	Model 3 + Model 4	21	-415069	162	0
6	Casualty Sex $\times$ Survivor Sex $\times$ Inside $\times$ Period	27	-414948	0	1

<sup>\*</sup>Period (3-level factor: Y0, Y1, Y2 in reference to casualty death), Inside (2-level factor: inside or outside of casualty's home range), Casualty Sex (2-level factor: male or female), Survivor Sex (2-level factor: male or female).

**Table 2.** 

		_	Male-Male			Female-Female			Male-Female		
Model	Variable	K	LL	ΔΒΙϹ	ω	LL	ΔΒΙϹ	ω	LL	ΔΒΙϹ	ω
1	None	4	-26524	1516	0	-178430	5538	0	-182879	6275	0
2	Inside $\times$ Period	9	-26051	622	0	-177124	2988	0	-182850	6281	0
3	$C_{age} \times Inside \times Period$	15	-26044	671	0	-176795	2404	0	-182221	5096	0
4	$C_{age} \times Inside \times Period$	15	-25885	353	0	-177097	3009	0	-181741	4137	0
5	Hunting $\times$ Inside $\times$ Period	15	-25978	540	0	-176991	2798	0	-182596	5847	0
6	Density $\times$ Inside $\times$ Period	15	-25940	463	0	-176999	2814	0	-181859	4372	0
7	Relatedness× Inside × Period	15	-25936	456	0	-175723	262	0	-182463	5581	0
8*	$C_{age} + S_{age}$	21	-25865	377	0	-176749	2388	0	-181122	2974	0
9*	$C_{age}$ + Hunting	21	-25961	570	0	-176741	2371	0	-182102	4935	0
10*	$C_{age} + Density$	21	-25921	490	0	-176750	2390	0	-181527	3783	0
11*	$C_{age} + Relatedness$	21	-25928	503	0	-175608	106	0	-181957	4644	0
12*	$S_{age}$ + Hunting	21	-25858	363	0	-176955	2800	0	-181407	3544	0
13*	$S_{age}$ + Density	21	-25847	341	0	-176968	2826	0	-180525	1780	0
14*	$S_{age}$ + Relatedness	21	-25685	18	0	-175712	315	0	-181497	3723	0
15*	Hunting + Density	21	-25898	443	0	-176915	2720	0	-181031	2792	0
16*	Hunting + Relatedness	21	-25828	302	0	-175700	290	0	-182226	5182	0
17*	Density + Relatedness	21	-25836	319	0	-175690	270	0	-181614	3957	0
18*	$C_{age} + S_{age} + Hunting$	27	-25837	384	0	-176691	2347	0	-180972	2749	0
19*	$C_{age} + S_{age} + Density$	27	-25838	386	0	-176702	2368	0	-180274	1353	0
20*	$C_{age} + S_{age} + Relatedness$	27	-25658	27	0	-175597	159	0	-181002	2809	0
21*	$C_{age}$ + Hunting + Density	27	-25857	425	0	-176705	2375	0	-180966	2737	0
22*	$C_{age}$ + Hunting + Relatedness	27	-25803	316	0	-175518	0	1	-181850	4505	0
23*	$C_{age}$ + Density + Relatedness	27	-25821	353	0	-175597	160	0	-181358	3521	0
24*	$S_{age}$ + Hunting + Density	27	-25803	316	0	-176876	2716	0	-179598	0	1
25*	$S_{age}$ + Hunting + Relatedness	27	-25645	0	0.98	-175688	341	0	-181210	3224	0
26*	$S_{age}$ + Density + Relatedness	27	-25675	61	0	-175680	324	0	-180447	1698	0
27*	Hunting + Density + Relatedness	27	-25782	274	0	-175649	263	0	-180901	2607	0
28*	$C_{age} + S_{age} + Hunting + Density$	33	-25768	310	0	-176654	2348	0	-179576	32	0
29*	$C_{age} + S_{age} + Hunting + Relatedness$	33	-25617	8	0.02	-175507	54	0	-180862	2604	0
30*	$C_{age} + S_{age} + Density + Relatedness$	33	-25654	82	0	-175586	212	0	-180231	1341	0
31*	$C_{age}$ + Hunting + Density + Relatedness	33	-25760	294	0	-175496	31	0	-180854	2588	0
32*	$S_{age}$ + Hunting + Density + Relatedness	33	-25629	31	0	-175638	316	0	-179580	39	0
33*	$C_{age} + S_{age} + Hunting + Density + Relatedness$	39	-25597	31	0	-175485	85	0	-179561	76	0

<sup>\*</sup>Model 8 to 33: Every variable is in a 3-way interaction with Inside × Period as shown in model 3. Bolded values are from the best models

#### Figure captions

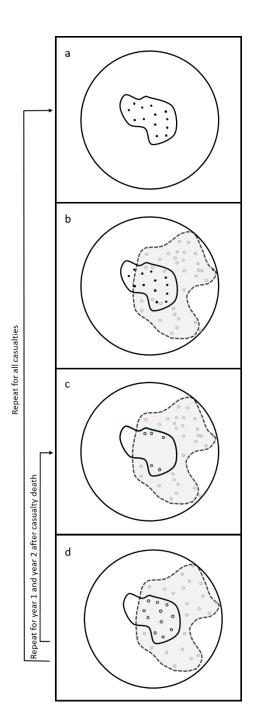
Figure 1. Schematic representation of data handling. For each brown bear casualty (panel a), we determined its 95% kernel HR and calculated a 40-km radius circular buffer centered on the HR centroid. We used (panel b) all GPS locations of the casualty (filled black points) and those belonging to surviving bears (open gray points) within the circular buffer to calculate a 95% kernel density isocline (shaded with dashed gray border), representing the sampling space, and (panel c) determined if the survivor relocations were inside (open black points) or outside (open gray points) the casualty's HR. We generated the same number of random (panel d) as real GPS locations and determined if the random locations were inside (open black points) or outside (open gray points) the casualty's HR. We repeated the same process (panel c and d) for the next two years using the same sampling space. We repeated the same process (panel a-d) for all casualties.

**Figure 2.** Log-odds ratios of brown bear survivors' use of a casualty's HR during the year in which the casualty died (Y0), the first (Y1) and second (Y2) year after the casualty's death for different casualty-survivor sex combinations. The dashed line is the baseline year (Y0) indicating the survivor's use of the casualty's HR before the casualty's death.

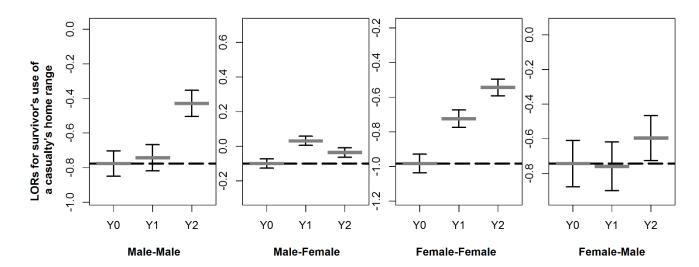
**Figure 3.** Log-odds ratios of nearby surviving brown bears' (survivors') use of hunter-killed bears' (casualties') HRs during the year in which the casualty died (Y0), the first year after the casualty's death (Y1), and the second year after its death (Y2) in response to casualty-survivor relatedness (panel a, b) and previous hunting intensity (panel c, d). Low and high values of relatedness and hunting intensities represent the 25<sup>th</sup> and 75<sup>th</sup> percentiles found in the male-male (panel a, c) and female-female (panel b, d) datasets. Note: the values on the y-axis are different among plots.

**Figure 4.** Log-odds ratios of surviving brown bears' (survivors') use of nearby hunter-killed bears' (casualties') home ranges during the year in which the casualty died in the fall (Y0), the first year after the casualty's death (Y1), and the second year after its death (Y2), in response to casualty and survivor age, density index, and hunting intensity. Low and high values represent the 25th and 75th percentiles of the variable for the respective casualty-survivor data set. Note: in panel b, young casualty and old casualty almost completely overlap one another at Y0; the scales and intervals are different among the plots.

# **Figure 1.**

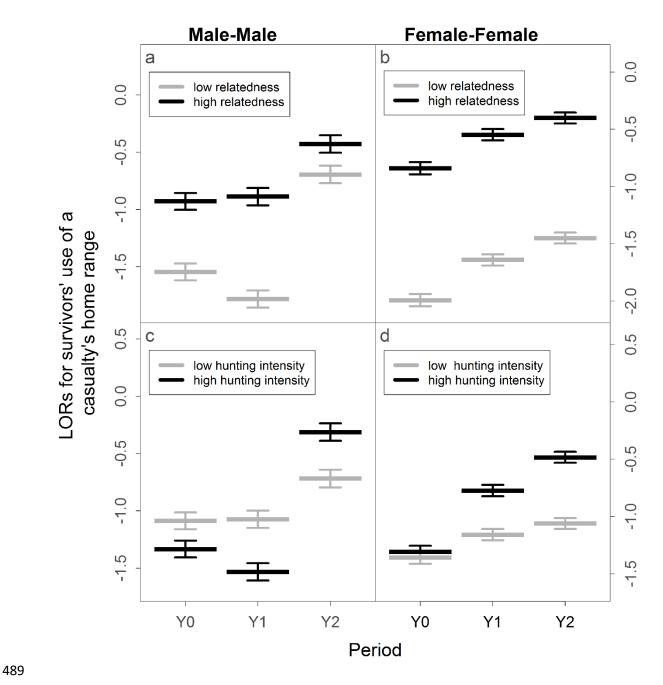


# **Figure 2.**

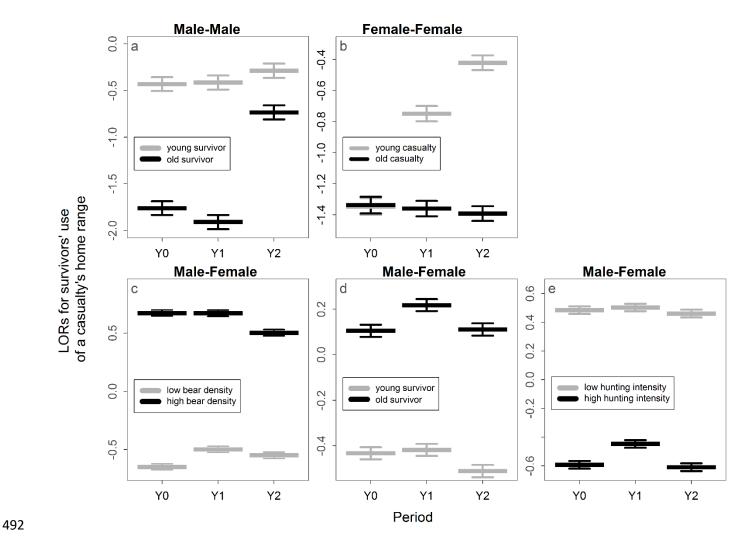


Sex combinations: casualty-survivor

# **Figure 3.**



# **Figure 4.**



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### 656 **Supporting Information**

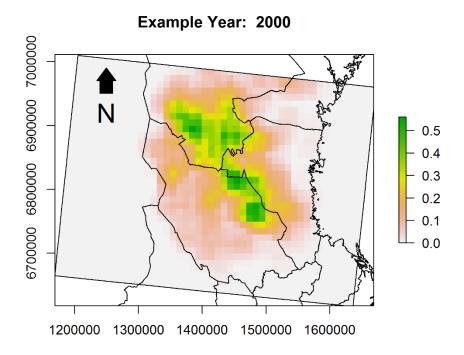
Additional Supporting Information may be found in the online version of this article:

- 659 **Appendix S1.** Annual bear density Index.
- **Table S1.** Summary statistics for microsatellites used for pedigree reconstruction.
- **Table S2**. Summary of parentage assignment from pedigree construction.
- **Table S3.** Parameter estimates of the best 'sex' model (Step I).
- Table S4. Parameter estimates of the best 'additional factors' model (Step II) for male-male casualty-
- 664 survivor combination.
- Table S5. Parameter estimates of the best 'additional factors' model (Step II) for female-female
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- Table S6. Parameter estimates of the best 'additional factors' model (Step II) for male-female casualty-
- 668 survivor combination.
- **Figure S1.** The distribution of relatedness estimates from Lynch-Ritland's (1999) estimator.
- Figure S2. Comparison of three isoclines (a: 95%; b: 90%; c: 75%) for the sampling spaces and respective
- 671 model results are shown for the sex-effect model, yielding similar results across isoclines.
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#### **SUPPORTING INFORMATION**

Appendix S1. Annual bear density index.

The annual bear density index was estimated using two sources of information: (1) individually identified bears, based on DNA in scats collected during organized efforts (available at http://rovbase.no; Bellemain *et al.* 2005) and (2) the Swedish Large Carnivore Observation Index (LCOI), both of which were collected during the fall hunting season (Kindberg, Ericsson & Swenson 2009). The latter information came from Swedish hunters, whose efforts covered virtually the entire areas of four counties of Gävleborg, Dalarna, Jämtland, and Västernorrland (for more details on collection efforts, see Kindberg, Ericsson & Swenson 2009). Scat collection data were used to create spatially explicit density index distributions, according to the county and the year in which an individual's scat collection took place.



We adopted the method of Jerina et al. (2013), by summing the weighted values of individual bear scat locations on a grid of 10 X 10 km cells, to account for the different number of samples among individuals. Grid cells were then smoothed with a 3x3 cell filter (i.e. a 30x30 km moving window) to derive county-specific density index distributions. Years of scat collection varied among counties. Thus, these maps were not directly comparable without an annual correction, for which we used the LCOI. The Swedish LCOI was initiated in 1998 by the Swedish Association for Hunting and Wildlife Management (Kindberg *et al.* 2011). Moose hunters report the number of bears they observe during the first week of moose hunting; the index is effort-corrected using hunter hours (Ericsson & Wallin 1999; Sylvén 2000). We approximated temporal trends in the LCOI for the period 1998-2015 for each county by fitting quadratic models using LCOI as the response and "year" plus year-squared as predictors. The latter term was used to smooth the relationship between year and the interannual LCOI values, which could vary substantially among years. Predicted LCOI values

from these models were then used to calculate a multiplicative annual correction factor (C) (**Eq. 1**), which was multiplied with each county's density distribution ( $d_i$ ) (**Eq. 2**).

$$C_{ij} = \frac{LCOI_{ij}}{LCOI_{scat \, year, i}}$$
 Eq. 1

Years in which scat was actually collected in a given county ( $i = scat \ year$ ) were given a correction factor of "1". Therefore, the annual density index (D) for a given county was derived using the following equation (Eq. 2) for the ith year, jth county, and the scat (collection) year.

$$D_{ij} = C_{ij} * d_j$$
 Eq. 2

County grids were then summed together by year to obtain the annual density index ( $D_i$ ) grid (a plot of  $D_{2000}$  is shown in the figure above using the UTM coordinate system: 'RT90 2.5 gon V'). The bear density index was extracted for each surviving bear's relocation in a given study period year (i.e., Y0, Y1, and Y2).

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Table S1. Summary statistics for microsatellites used for pedigree reconstruction and Lynch and Ritland's (1999) relatedness index for brown bears (N = 1,614) in southcentral Sweden.  $N_A$ : Number of alleles,  $H_o$ : observed heterozygosity,  $H_e$ : expected heterozygosity,  $P_{ex}$ : probability of exclusion for a single unknown parent,  $P_{id}$ : probability of identity for unrelated individuals.

Locus	$N_A$	Ho	He	Pex	P <sub>id</sub>
G1A <sup>a</sup>	6	0.625	0.630	0.380	0.810
$G1D^a$	7	0.592	0.620	0.340	0.786
G10B <sup>a</sup>	8	0.699	0.703	0.442	0.855
G10C <sup>b</sup>	5	0.697	0.698	0.460	0.864
$G10J^{c}$	6	0.574	0.570	0.325	0.762
G10H <sup>c</sup>	9	0.525	0.545	0.308	0.740
G10L <sup>a</sup>	8	0.757	0.760	0.544	0.905
G10O <sup>a</sup>	3	0.392	0.397	0.166	0.564
$G10P^b$	6	0.736	0.757	0.535	0.902
$Mu05^d$	8	0.640	0.636	0.365	0.797
$Mu10^d$	8	0.806	0.806	0.610	0.933
Mu15 <sup>d</sup>	4	0.658	0.643	0.364	0.805
Mu23 <sup>d</sup>	8	0.709	0.699	0.485	0.876
$Mu50^d$	10	0.735	0.756	0.538	0.903
Mu51 <sup>d</sup>	9	0.824	0.796	0.592	0.926
Mu61 <sup>d</sup>	4	0.529	0.542	0.272	0.714
average	7	0.656	0.660	0.420	0.821

<sup>&</sup>lt;sup>a</sup>Paetkau and Strobeck (1994); <sup>b</sup>Paetkau *et al.* (1995); <sup>c</sup>Paetkau, Shields and Strobeck (1998); <sup>d</sup>Taberlet *et al.* (1997).

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Table S2. Summary of parentage assignment from pedigree construction using Cervus 2.0 (initial assessment; Marshall *et al.* 1998; Kalinowski, Taper & Marshall 2007)) and Colony 3.0 (sibship reconstruction and recovery of further father assignments; Jones & Wang 2010). Only some mothers were known (not fathers) during assignment, with the rest based on genetics.

Parentage Assignment	Count	Proportion of Offspring	
Offspring sample size	1463	NA	
Maternity of offspring			
Known mothers	321	0.22	
Assigned mothers with genetics alone	455	0.31	
Total Assigned mothers	776	0.53	
Paternity of offspring			
Assigned fathers (known genotypes)	666	0.46	
Assigned fathers (reconstructed genotypes*)	68	0.05	
Total assigned fathers	734	0.50	

<sup>\*</sup>Colony 3.0 reconstructed sibship across known and reconstructed father genotypes. The latter is shown on a separate line.

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Table S3. Parameter estimates of the best sex-effect model (Step I; Model 6 in Table 1).

Variable	β	95 % Confidence intervals	
		Lower	Upper
Intercept	0.075	0.054	0.095
Survivor $Sex = M$	-0.012	-0.050	0.026
Casualty $Sex = M$	-0.034	-0.065	-0.002
Inside = True	-0.984	-1.034	-0.933
Period = Y1	-0.012	-0.032	0.008
Period = Y2	-0.025	-0.045	-0.006
Survivor Sex = $M \times Casualty Sex = M$	0.215	0.158	0.272
$Inside = True \times Period = Y1$	0.259	0.192	0.327
$Inside = True \times Period = Y2$	0.440	0.377	0.503
Survivor Sex = $M \times Inside = True$	0.240	0.118	0.361
Survivor Sex = $M \times Period = Y1$	0.010	-0.041	0.061
Survivor Sex = $M \times Period = Y2$	0.017	-0.033	0.066
Casualty $Sex = M \times Inside = True$	0.883	0.826	0.940
Casualty $Sex = M \times Period = Y1$	-0.043	-0.075	-0.012
Casualty $Sex = M \times Period = Y2$	-0.001	-0.032	0.030
$Survivor\ Sex = M \times Inside = True \times Period = Y1$	-0.275	-0.435	-0.116
$Survivor\ Sex = M \times Inside = True \times Period = Y2$	-0.293	-0.443	-0.142
$Casualty \ Sex = M \times Inside = True \times Period = Y1$	-0.128	-0.205	-0.051
$Casualty \ Sex = M \times Inside = True \times Period = Y2$	-0.376	-0.448	-0.304
$Survivor \ Sex = M \times Casualty \ Sex = M \times Inside = True$	-0.916	-1.055	-0.776
Survivor Sex = $M \times Casualty Sex = M \times Period = Y1$	0.038	-0.041	0.117
Survivor Sex = $M \times Casualty Sex = M \times Period = Y2$	-0.080	-0.157	-0.003
$Survivor \ Sex = M \times Casualty \ Sex = M \times Inside = True \times$			
Period = Y1	0.177	-0.003	0.357
$Survivor \ Sex = M \times Casualty \ Sex = M \times Inside = True \times$			
Period = Y2	0.577	0.404	0.750

Table S4. Parameter estimates of the best 'additional factors' model (Step II) for male-male casualty-survivor combination (Model 25 for male-male data set from Table 2).

Variable	β	95 % Confidence intervals	
		Lower	Upper
Intercept	0.256	0.167	0.346
Survivor Age	0.033	-0.048	0.114
Hunting	-0.081	-0.172	0.010
Relatedness	-0.063	-0.131	0.004
Inside = TRUE	-1.194	-1.292	-1.097
Period = Y1	-0.017	-0.077	0.043
Period = Y2	-0.091	-0.153	-0.029
$Inside = TRUE \times Period = Y1$	-0.079	-0.221	0.064
$Inside = TRUE \times Period = Y2$	0.651	0.527	0.775
Survivor Age $\times$ Inside = TRUE	-1.279	-1.497	-1.060
Survivor Age $\times$ Period = Y1	0.010	-0.065	0.084
Survivor Age $\times$ Period = Y2	0.020	-0.054	0.094
$Hunting \times Inside = TRUE$	-0.172	-0.282	-0.062
$Hunting \times Period = Y1$	0.045	-0.025	0.114
$Hunting \times Period = Y2$	-0.094	-0.170	-0.017
Relatedness $\times$ Inside = TRUE	0.598	0.497	0.699
Relatedness $\times$ Period = Y1	-0.065	-0.125	-0.004
Relatedness $\times$ Period = Y2	0.021	-0.040	0.082
Survivor Age $\times$ Inside = TRUE $\times$ Period = Y1	-0.159	-0.459	0.141
Survivor Age $\times$ Inside = TRUE $\times$ Period = Y2	0.850	0.606	1.093
$Hunting \times Inside = TRUE \times Period = Y1$	-0.150	-0.302	0.003
$Hunting \times Inside = TRUE \times Period = Y2$	0.456	0.311	0.601
$Relatedness \times Inside = TRUE \times Period = Y1$	0.271	0.134	0.407
Relatedness $\times$ Inside = TRUE $\times$ Period = Y2	-0.341	-0.470	-0.211

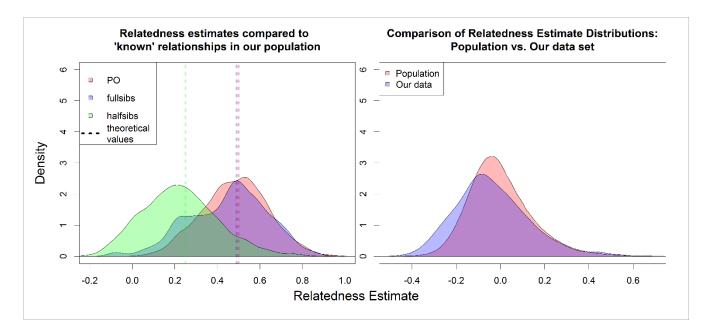
Table S5. Parameter estimates of the best 'additional factors' model (Step II) for female-female casualty-survivor combination (Model 22 for female-female data set from Table 2).

Variable	β	95 % Confidence intervals	
		Lower	Upper
Intercept	0.070	0.048	0.091
Casualty Age	0.006	-0.016	0.027
Hunting	-0.001	-0.023	0.021
Relatedness	-0.046	-0.064	-0.027
Inside = TRUE	-1.342	-1.405	-1.278
Period = Y1	-0.015	-0.035	0.004
Period = Y2	-0.029	-0.048	-0.009
$Inside = TRUE \times Period = Y1$	0.318	0.234	0.402
$Inside = TRUE \times Period = Y2$	0.483	0.400	0.567
Casualty Age $\times$ Inside = TRUE	0.004	-0.052	0.061
Casualty Age $\times$ Period = Y1	0.019	-0.001	0.039
Casualty Age $\times$ Period = Y2	0.029	0.009	0.049
$Hunting \times Inside = TRUE$	0.028	-0.030	0.087
$Hunting \times Period = Y1$	0.002	-0.018	0.023
$Hunting \times Period = Y2$	0.004	-0.016	0.025
$Relatedness \times Inside = TRUE$	0.823	0.767	0.879
Relatedness $\times$ Period = Y1	-0.013	-0.034	0.007
Relatedness $\times$ Period = Y2	-0.017	-0.037	0.004
Casualty Age $\times$ Inside = TRUE $\times$ Period = Y1	-0.305	-0.383	-0.227
Casualty Age $\times$ Inside = TRUE $\times$ Period = Y2	-0.482	-0.561	-0.403
$Hunting \times Inside = TRUE \times Period = Y1$	0.194	0.112	0.275
$Hunting \times Inside = TRUE \times Period = Y2$	0.305	0.224	0.385
$Relatedness \times Inside = TRUE \times Period = Y1$	-0.042	-0.118	0.034
$Relatedness \times Inside = TRUE \times Period = Y2$	-0.074	-0.149	0.001

Table S6. Parameter estimates of the best 'additional factors' model (Step II) for male-female casualty-survivor combination (Model 24 for female-female data set from Table 2).

Variable	β	95 % Confidence intervals	
		Lower	Upper
Intercept	-0.011	-0.058	0.036
Hunting	0.237	0.187	0.286
Survivor Age	-0.213	-0.256	-0.170
Density	-0.320	-0.370	-0.271
Inside = TRUE	-0.061	-0.090	-0.032
Period = Y1	-0.032	-0.057	-0.006
Period = Y2	0.017	-0.010	0.043
$Inside = TRUE \times Period = Y1$	0.083	0.045	0.121
$Inside = TRUE \times Period = Y2$	-0.020	-0.059	0.019
$Hunting \times Inside = TRUE$	-0.442	-0.473	-0.412
$Hunting \times Period = Y1$	-0.030	-0.059	-0.002
$Hunting \times Period = Y2$	-0.009	-0.038	0.020
Survivor Age $\times$ Inside = TRUE	0.443	0.414	0.471
Survivor Age $\times$ Period = Y1	-0.058	-0.085	-0.031
Survivor Age $\times$ Period = Y2	-0.043	-0.070	-0.016
Density $\times$ Inside = TRUE	0.651	0.620	0.681
Density $\times$ Period = Y1	0.028	0.000	0.055
Density $\times$ Period = Y2	0.053	0.025	0.081
$Hunting \times Inside = TRUE \times Period = Y1$	0.052	0.012	0.092
$Hunting \times Inside = TRUE \times Period = Y2$	0.003	-0.038	0.044
Survivor Age $\times$ Inside = TRUE $\times$ Period = Y1	0.081	0.043	0.119
Survivor Age $\times$ Inside = TRUE $\times$ Period = Y2	0.069	0.031	0.108
$Density \times Inside = TRUE \times Period = Y1$	-0.075	-0.116	-0.034
$Density \times Inside = TRUE \times Period = Y2$	-0.132	-0.174	-0.091

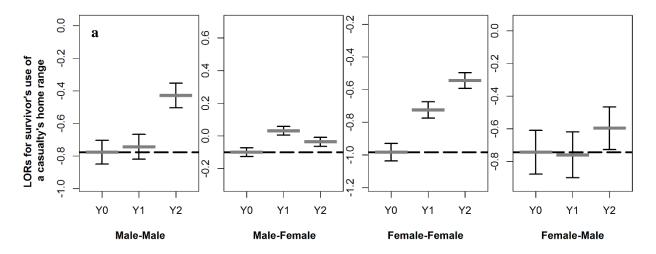
Figure S1. *Left panel*: The distribution of relatedness estimates from Lynch-Ritland's (1999) estimator compared to theoretical values from known relationships (PO = parent-offspring, full sibs, and half sibs) *Right panel*: The comparison between the estimated Lynch-Ritland's (1999) values of all brown bears we have genetic data on in the Scandinavian Brown Bear Research Project (SBBRP) and those used in our study sample. Mean values of Lynch-Ritland estimates are similar to theoretical values, and our sample is comparable to the population of Lynch-Ritland values for all bears in the SBBRP.



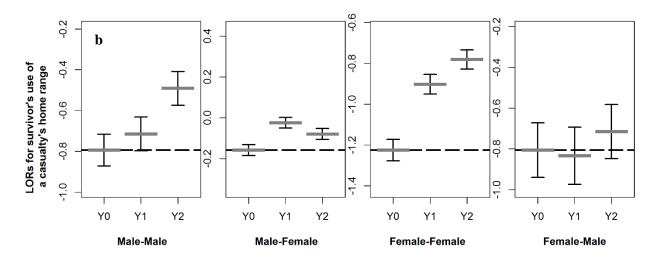
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Lynch, M. & Ritland, K. (1999) Estimation of Pairwise Relatedness With Molecular Markers. *Genetics*, **152**, 1753-1766.

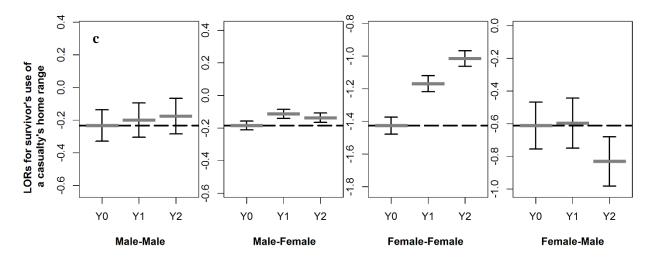
Figure S2. Log-odds ratio (LOR; y-axis) of surviving brown bears' (survivors') use of nearby hunter-killed bears' (casualties') home ranges during the year in which the casualty died in the fall (Y0), the first year after the casualty's death (Y1), and the second year after its death (Y2), according to the sex combination of casualty-survivors. Comparison of the three isoclines (a: 95%; b: 90%; c: 75%) of the sampling spaces are shown, yielding similar results. The spatial response of male-male disappears as the sampling space is reduced to 75% isocline, which is the sex that depicts more extensive ranging behavior.



Sex combinations: casualty-survivor



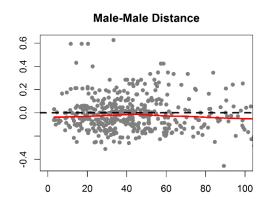
Sex combinations: casualty-survivor

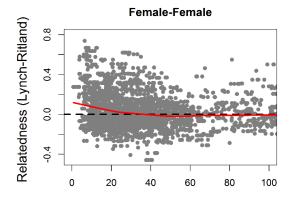


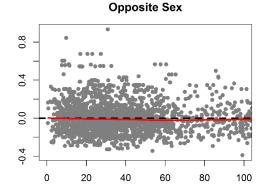
Sex combinations: casualty-survivor

Figure S3. Pairwise relatedness (Lynch & Ritland 1999) plotted against distances between home range centroids of brown bears. Separate plots are shown for pairings between males (n = 948), females (n = 5086), and bears of the opposite sex (n = 4428). Gray dots are the raw data and red lines are plotted using LOWESS curves, providing nearly identical to the findings of Støen *et al.* (2005). Female pairings of higher relatedness are correlated with smaller distances between home range centroids, but there is no evidence of such a pattern for male pairings or those of the opposite sex.

## Distance between home range centroids







Distance (km) between home range centroids

## References

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Figure S3. Proportion of home range overlap between individual females and their female neighbors against individual female age. Fitted values from a generalized additive model (red line) shows no significant relationship (smoother function: p = 0.343) between female-female home range overlap with a basis in female age (n = 752).

# Individual female and female neighbor overlap against individual female age

